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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=10; day=17; hr=14; min=7; sec=33; ms=914;]

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Application No: 09541094 Version No: 1.0

Input Set:

Output Set:

Started: 2008-10-17 13:50:27.890
Finished: 2008-10-17 13:50:29.731
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 841 ms
Total Warnings: 18
Total Errors: 2
No. of SeqIDs Defined: 19
Actual SeqID Count: 19

Error code	Error Description
W 251	Found intentionally skipped sequence in SEQID (1)
W 251	Found intentionally skipped sequence in SEQID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 249	Order Sequence Error <210> -> <220>; Expected Mandatory Tag: <211> in SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)

Input Set:

Output Set:

Started: 2008-10-17 13:50:27.890
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Total Errors: 2
No. of SeqIDs Defined: 19
Actual SeqID Count: 19

Error code	Error Description
E 250	Structural Validation Error; Sequence listing may not be indexable

SEQUENCE LISTING

<110> St. George-Hyslop, Peter H.
Fraser, Paul E.
University of Toronto

<120> A novel presenilin associated membrane
protein and uses thereof

<130> 1034/1F812-US1

<160> 19

<170> FastSEQ for Windows Version 3.0

<210> 1

<400> 1

000

<210> 2

<400> 2

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<210> 3

<211> 422

<212> DNA

<213> mouse

<400> 3

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<211> 473

<212> DNA

<213> unknown

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<223> EST from unknown organism

<400> 4

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ctagtgtgca	gtgccccaaat	gatgggttg	gtaattactc	caactcctac	gggccagagt	360

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<210> 6

<211> 463

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<213> unknown

<220>

<223> EST from unknown organism

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catggtttca gtcgatcctg aaacatgacc taaggtccta tttggatgac aggccctttc 360
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<211> 481

<212> DNA

<213> unknown

<220>

<223> EST from unknown organism

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<211> 398

<212> DNA

<213> unknown

<220>

<223> EST from unknown organism

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<211> 172
<212> DNA
<213> unknown

<220>
<223> EST from unknown organism

<400> 9

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<211> 425
<212> DNA
<213> unknown

<220>
<223> EST from unknown organism

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<212> DNA
<213> C. Elegans

<400> 11

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<211> 721

<212> PRT

<213> C. Elegans

<400> 12

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Asn Ala Cys Tyr Arg Thr Phe Asn Lys Thr His Glu Phe	Gly Cys Gln
35 40 45	
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50 55 60	
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65 70 75 80	
Tyr Ser Gly Lys Tyr Trp Ala Leu Leu Pro Val Asn Leu	Ile Arg Arg
85 90 95	
Asp Thr Ile Ser Gln Leu Lys Ser Ser Lys Cys Leu Ser	Gly Ile Val
100 105 110	
Leu Tyr Asn Ser Gly Glu Ser Ile His Pro Gly Asp Glu	Ser Thr Ala
115 120 125	
Ala Ser His Asp Ala Glu Cys Pro Asn Ala Ala Ser Asp	Tyr Tyr Leu
130 135 140	
Gln Asp Lys Asn Glu Glu Tyr Cys Glu Arg Lys Ile Asn	Ser Arg Gly
145 150 155 160	
Ala Ile Thr Arg Asp Gly Leu Met Lys Ile Asp Trp Arg	Ile Gln Met
165 170 175	
Val Phe Ile Asp Asn Ser Thr Asp Leu Glu Ile Ile Glu	Lys Cys Tyr
180 185 190	
Ser Met Phe Asn Lys Pro Lys Glu Asp Gly Ser Ser Gly	Tyr Pro Tyr
195 200 205	
Cys Gly Met Ser Phe Arg Leu Ala Asn Met Ala Ala Gly	Asn Ser Glu
210 215 220	
Ile Cys Tyr Arg Arg Gly Lys Asn Asp Ala Lys Leu Phe	Gln Met Asn
225 230 235 240	
Ile Asp Ser Gly Asp Ala Pro Gln Leu Cys Gly Ala Met	His Ser Asp
245 250 255	
Asn Ile Phe Ala Phe Pro Thr Pro Ile Pro Thr Ser Pro	Thr Asn Glu
260 265 270	
Thr Ile Ile Thr Ser Lys Tyr Met Met Val Thr Ala Arg	Met Asp Ser
275 280 285	
Phe Gly Met Ile Pro Glu Ile Ser Val Gly Glu Val Ser	Val Leu Thr
290 295 300	
Ser Ile Ile Ser Val Leu Ala Ala Ala Arg Ser Met Gly	Thr Gln Ile
305 310 315 320	
Glu Lys Trp Gln Lys Ala Ser Asn Thr Ser Asn Arg Asn	Val Phe Phe
325 330 335	
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Val Asp Gly Glu Arg Tyr Gln Gln Asn Lys Thr Gln Thr Asp Arg Val		
405	410	415
Ile Asp Arg Ile Glu Arg Gly Leu Arg Ser His Ala Phe Asp Leu Glu		
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Lys Pro Ser Gly Ser Gly Asp Arg Val Pro Pro Ala Ser Trp His Ser		
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Phe Ala Lys Ala Asp Ala His Val Gln Ser Val Leu Leu Ala Pro Tyr		
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Gly Lys Glu Tyr Glu Tyr Gln Arg Val Asn Ser Ile Leu Asp Lys Asn		
465	470	475
Glu Trp Thr Glu Asp Glu Arg Glu Lys Ala Ile Gln Glu Ile Glu Ala		
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Val Ser Thr Ala Ile Leu Ala Ala Ala Asp Tyr Val Gly Val Glu		
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Thr Asp Glu Val Val Ala Lys Val Asp Lys Lys Leu Ile Thr Thr Ile		
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Gln Lys Leu Asp Gly Gly Arg Tyr His Lys Leu Phe Asn Ser Tyr Gly		
545	550	555
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565	570	575
Pro Thr Val Leu His Trp Leu Thr Ile Phe Ala Leu Gly Ser Asp Lys		
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Phe Gln Ala Met Tyr Thr Tyr Thr Trp Gln Pro Asn Pro Tyr Thr Gly		
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Asn Phe Ser Cys Leu Lys Ser Ala Ile Val Lys Lys Val Met Val Ser		
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645	650	655
Ser Thr Trp Met Glu Ser Val Tyr Ile Ile Glu Ser Val Asn Leu Tyr		
660	665	670
Leu Met Glu Asp Ala Ser Phe Glu Tyr Thr Met Ile Leu Ile Ala Val		
675	680	685
Ile Ser Ala Leu Leu Ser Ile Phe Ala Val Gly Arg Cys Ser Glu Thr		
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Leu		

<210> 13
 <211> 2949
 <212> DNA
 <213> human

<400> 13

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